The Proteomics Platform aims to provide support and technical advisory services in the field of proteomics, both for researchers at public centers and the private sector, as well as conducting its own and participating in joint projects.

The Platform offers technology to carry out mass spectrometry analysis, from determining molecular mass through complex proteomic analyses like quantifying the level of protein expression.

The unit has latest-generation facilities and qualified personnel to carry out the services it offers and kick off new projects. Moreover, the unit is part of ProteoRed-ISCIII, the Spanish proteomics network that promotes new technology and excellence in service offered by member laboratories.

The Proteomics Technology Platform is committed to providing personalized, quality, confidential service, with open communication and flexibility.

The Platform carries out a wide range of activities related with identifying proteins and analyzing differential protein expression, including:

**Enzymatic digestion of proteins.** Depending on the primary sequencing of the protein, different enzymes can be used to obtain the right peptides to be analyzed using mass spectrometry.

**Identifying proteins through enzymatic digestion, analysis with mass spectrometry and search in database** (the laboratory has MASCOT and Sequest search engines and Proteome Discoverer and Peaks Studio software as well as access to the Phenx search engine on a private server)
- Peptide fingerprinting and fragmentation mass spectrometry (MALDI-fingerprinting-MS/MS). Used to identify pure proteins and 2-DE gel staining.
- Separating peptides using liquid chromatography and mass spectrometry (LC-MS/MS). Used to identify proteins in samples with moderate complexity in terms of number of proteins.

**Identifying and quantifying relative level of protein expression with mass spectrometry** (LC-MS/MS).
- Labeling with stable isobars (iTRAQ). Allows comparison of up to 8 samples.
- Label-free.

**Identifying and profiling post-translational modifications (PTMs) in proteins** (LC-MS/MS).
- Phosphorylation with or without titanium dioxide phosphopeptide enrichment (TiO2).
- Acetylation, methylation.

**Sequencing peptides using mass spectrometry** (MS/MS). This method can be used to obtain the full or partial amino-acid sequencing of peptides. Used with peptides under 3000 Da.

**Determining molecular mass using mass spectrometry** (MALDI-TOF MS). Applies to profiling molecular mass of molecules through mass spectrometry.

**Sample preparation**
- Precipitating proteins in order to obtain protein extracts not contaminated with salts or lipids.
- Quantifying total proteins using Bradford or similar.
- Removing interference with specific filters, membranes, cartridges and/or columns.

**Separating proteins using two-dimensional electrophoresis** (2-DE). Depending on the complexity and number of samples, 2-DE can be mini (8x7 cm) or large (20x20 cm).

**Self-service gel imaging.** Used to compare protein patterns and profile relative abundance of proteins in different samples.

**Guidance for self-service users** of two-dimensional electrophoresis and mass spectrometry. Access and technical advice for public and private groups lacking the facilities to carry out 2-DE experiments and MALDI-TOF mass spectrometry in their laboratories.